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23 140 4.9 255 1 41BB_HUMAN 4-1BB LIGAND RECEPTOR 9.85e-08
24 141 4.9 277 7 OX40_HUMAN OX40L RECEPTOR PRECUR 6.62e-08
25 137 4.8 327 3 FASA_MOUSE FAST RECEPTOR PRECURS 3.22e-07
26 134 4.7 250 2 CD27_MOUSE CD27L RECEPTOR PRECUR 1.04e-06
27 134 4.7 335 3 FASR_HUMAN FASL RECEPTOR PRECURS 1.04e-06
28 124 4.3 103 10 VA53_VACC PROTEIN A53. 4.67e-05
29 124 4.3 103 10 VA53_VACCY PROTEIN A53. 4.67e-05
30 115 4.0 360 11 XI19_YEAST HYPOTHETICAL 41.6 KD 1.24e-03
31 110 3.8 535 3 D2_DICDI CAMP-REGULATED D2 PRO 7.20e-03
32 105 3.7 2813 10 VWF_HUMAN VON WILLEBRAND FACTOR 3.96e-02
33 102 3.6 3084 6 LM1_MOUSE LAMININ ALPHA 1 CHAIN 1.07e-01
34 101 3.5 712 4 GFAL_CANAL GLUCOSAMINE--FRUCTOSE 1.49e-01
35 101 3.5 1122 11 YGIC_YEAST HYPOTHETICAL 128.8 KD 1.49e-01
36 100 3.5 1752 3 DESP_HUMAN DESMOLAKIN I AND II 2.05e-01
37 99 3.5 2670 11 YA05_SCHEO PHOSPHATE REGULON SEN 7.33e-01
38 96 3.4 431 7 PR07_SHIDY PRE-MRNA SPLICING FAC 3.90e-01
39 98 3.4 494 7 PR11_YEAST SYF_YEAST VALYL-TRNA SYNTHETASE 7.33e-01
40 96 3.4 1104 9 XCPE_XENIA CHROMOSOME ASSEMBLY P 7.33e-01
41 96 3.4 1203 10 KAB7_YEAST PROBABLE SERINE/THREO 7.33e-01
42 96 3.4 1356 5 MYSC_CABEL MYOSIN HEAVY CHAIN C 3.90e-01
43 98 3.4 1947 6 PGFM_MOUSE BASEMENT MEMBRANE-SPE 7.33e-01
44 96 3.4 3707 7 DYHC_ELAST DYNIN HEAVY CHAIN, C 5.36e-01
45 97 3.4 4092 3
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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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**MPSICH\_PP** protein - protein database search, using Smith-Waterman algorithm  
 on: Wed Aug 20 09:54:07 1997; MasPar time 12.22 Seconds  
 Tabular output not generated.

Title: >US-08-469-637A-2  
 Description: (22-401) from US08469637A1.pep (2 of 2)  
 Perfect Score:  
 Sequence: 1 ETFPKVLHYDEBTSHOLLC.....OKLFLEMIGNOVQSVKISCL 380

Scoring table: PAM 150  
 Gap 11

Searched: 59021 seqs., 21210388 residues  
 Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot34  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.034; Variance 81.732; scale 0.588

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

No.	Score	Query Length	DB ID	Description	Pred. No.
1	405	14.2	461 9	TNR2_HUMAN TUMOR NECROSIS FACTOR	6.30e-63
2	375	13.1	474 9	TNR2_MOUSE TUMOR NECROSIS FACTOR	3.56e-55
3	303	10.6	277 2	CD40_HUMAN CD40 RECEPTOR PRECUR	2.64e-40
4	294	10.3	289 2	CD40_MOUSE CD40 RECEPTOR PRECUR	2.31e-38
5	269	9.4	326 10	VT2_MXVLTUMOR NECROSIS FACTOR	5.03e-33
6	265	9.3	415 9	TNRC_MOUSE LIMPROTOKIN-BETA RECE	3.52e-32
7	260	9.1	325 10	TUMOR NECROSIS FACTOR	3.98e-31
8	260	9.1	435 9	TNRC_HUMAN LIMPHOMOXIN-BETA RECE	3.98e-31
9	230	8.0	349 10	VC22_VARV PROTEIN C22/B28_HOMO	6.59e-25
10	221	7.7	454 9	FASL RECEPTOR PRECURS	4.45e-23
11	220	7.7	461 9	TUMOR NECROSIS FACTOR	7.09e-23
12	215	7.5	416 6	TRI_RAT TUMOR NECROSIS FACTOR	3.67e-16
13	213	7.4	427 6	NGF_CHICK LOW-AFFINITY NERVE GR	7.20e-22
14	207	7.2	425 6	NGFR_RAT LOW-AFFINITY NERVE GR	1.81e-21
15	188	6.5	323 3	FASL RECEPTOR PRECURS	1.51e-16
16	186	6.5	461 9	TNRL_PIG TUMOR NECROSIS FACTOR	4.45e-23
17	178	6.2	595 2	CDB30_HUMAN CD30L RECEPTOR PRECUR	1.24e-14
18	172	6.0	455 9	TNRI_HUMAN TUMOR NECROSIS FACTOR	1.67e-13
19	159	5.6	256 1	41BB_MOUSE 4-1BB LIGAND RECEPTOR	4.22e-11
20	159	5.6	CDD7_HUMAN CD27L RECEPTOR PRECUR	4.22e-11	
21	146	5.1	271 7	OX40_RAT OX40 RECEPTOR PRECUR	8.91e-08
22	144	5.0	272 7	OX40_MOUSE OX40L RECEPTOR PRECUR	2.00e-08

### ALIGNMENTS

RESULT ID TNR2\_HUMAN STANDARD: PRT: 461 AA.

AC P20353; DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)

DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TNFR2) (P20) (TNF-R2) (CD120B).

GN TNFR2 OR TNFR.

OS HOMO\_SAPIENS (HUMAN)

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

[1]

RN SEQUENCE FROM N.A.

RX MEDLINE; 90260639.

RX SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R.,

RX DOWER S.K., COSMAN D., GOODWIN R.G.; SCIENCE 248:1019-1023(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE; 9104591.

RX KOHNO T., BREWER M.T., BARKER S.L., SCHWARTZ P.E., KING M.W.,

RX HALE K.K., SQUIRES C.H., THOMSON R.C., VANNICE J.L.;

RX PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).

RX SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE; 90349572.

RX HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,

RX RINGOLD G.M., PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).

RX SEQUENCE OF 27-31.

RX MEDLINE; 90110235.

RX ENGELMANN H., NOVICK D., WALLACH D.;

RX J. BIOL. CHEM. 265:1531-1536(1990).

RX [5]

RX SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362.

RX MEDLINE; 91056048.

RX LOETSCHER H., SCHLAGER B.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,

RX BROCKHAUS M.;

RX J. BIOL. CHEM. 265:20131-20138(1990).

RX [6]

RX CHARACTERIZATION.

RX MEDLINE; 9301640.

RX PENNICA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,

RX LIPIAT M.T., GODDEL D.V.;



OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RA EUTHERIA; PRIMATES.  
 RN [1] SEQUENCE FROM N A.  
 RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 RX MEDLINE: 89356608.  
 RA STAMENKOVIC I., CLARK E.A., SEED B.;  
 RL EMBO J. 8:1403-1410(1989).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: X60592; G39591; -.  
 DR PIR: S04460; S04460.  
 DR MIM: 109535; -.  
 DR PROSITE; PS00652; TNFR\_NGFR.  
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 277 CD40 RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 216 277 4 X TNFR-CYS.  
 FT DOMAIN 25 187 TNFR-CYS 1.  
 FT REPEAT 25 60 TNFR-CYS 2.  
 FT REPEAT 61 103 TNFR-CYS 3.  
 FT REPEAT 103 144 TNFR-CYS 3.  
 FT REPEAT 144 187 TNFR-CYS 4.  
 FT REPEAT 145 153 POTENTIAL.  
 FT CARBOHYD 180 180 POTENTIAL.  
 FT CARBOHYD 180 180 POTENTIAL.  
 SQ SEQUENCE 277 AA; 3B28411 CRC32;  
  
 Query Match 10.6%; Score 303; DB 2; Length 277;  
 Best Local Similarity 36.8%; Pred. No. 2.54e-40;  
 Matches 56; Conservative 21; Mismatches 67; Indels 8; Gaps 7;  
  
 Db 38 csicggqkqyvsdcfeetecipcgseseftlwnrthchqkycapn-lgir-vqgk 95  
 QY 41 CDKCPPEIYLQHCTAKWKTVCAPCPHYDWSHTSDEC-L-YCPVCKELQVYQEC 97  
  
 Db 96 tsetdtlotccgwhatseacescvlhrcspqfgykq1atqysdticepcpgffsnvs 155  
 QY 98 NRTHNRVCECKEGRY-L-EI-EFCLKHRSRCPGGFGVVOAGTPERNVTCKRCPDGFESNET 154  
  
 Db 156 safekchpwtsctekd1vvqgegtntkadvcg 187  
 QY 155 SSKAPCRKHTNCVFGILLTOKGNATHDNC 186  
  
 CULT 4 STANDARD; PRT; 289 AA.  
 AC P27512;  
 DT 01-AUG-1992 (REL. 23, CREATED)  
 DT 01-OCT-1995 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1995 (REL. 34, LAST ANNOTATION UPDATE)  
 DE CD40 RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC BUTHERIA; RODENTIA.  
 RN [1] SEQUENCE FROM N A.  
 RP SEQUENCE FROM N A.  
 RX MEDLINE: 92105763.  
 RA TORRES R.M., CLARK E.A.;  
 RL J. IMMUNOL. 148:620-626(1992).  
 RP REVISONS.  
 RC STRAIN-BALB/C;  
 RA TORRES R.M.;  
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDJB DATA BANKS.  
 RN [3] SEQUENCE FROM N A.  
 RP STRAIN-BALB/C; TISSUE=LIVER;  
 RX MEDLINE: 93094586.  
 RA GRIMALDI J.C., TORRES R., KOZAK C.A., CHANG R., CLARK E.A.,  
  
 RA HOWARD M., COCKAYNE D.A.;  
 RL J. IMMUNOL. 149:3521-3526(1992).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: M03312; G155359; -.  
 DR EMBL: M4126; G193526; JOINED.  
 DR EMBL: M24128; G193526; JOINED.  
 DR EMBL: M9417; G193526; JOINED.  
 DR PIR: A46776; A46476.  
 DR HSSP; P19438; 1TNR.  
 DR PROSITE; PS00652; TNFR\_NGFR.  
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 289 CD40 RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 216 289 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 POTENTIAL.  
 FT CARBOHYD 153 153 POTENTIAL.  
 SQ SEQUENCE 289 AA; 3B270A2C CRC32;  
  
 Query Match 10.3%; Score 294; DB 2; Length 289;  
 Best Local Similarity 38.8%; Pred. No. 2.31e-38;  
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;  
  
 Db 38 cdicqpggrlltsctalktqkpcpsgsgefaqswnrestrchqkhepn-qgir-vkreg 95  
 QY 41 CDKCPPEIYLQHCTAKWKTVCAPCPHYDWSHTSDEC-L-YCPVCKELQVYQEC 97  
  
 Db 96 taesdtvctckeqhtskdcacqahpcipafgvymenattttvchpcpgffsnvs 155  
 QY 98 NRTHNRVCECKEGRY-L-EI-EFCLKHRSRCPGGFGVVOAGTPERNVTCKRCPDGFESNET 154  
  
 Db 156 slfekchpwtsctekd1vvqgegtntkadvcg 187  
 QY 155 SSKAPCRKHTNCVFGILLTOKGNATHDNC 186  
  
 RESULT 5 STANDARD; PRT; 326 AA.  
 ID VT2.MYXVL  
 ID P29825;  
 AC P29825;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).  
 GN T2.  
 OS MYXOMA VIRUS (STRAIN LAUSANNE).  
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;  
 OC LEPORIPOVIRINAE.  
 RN [1] SEQUENCE FROM N A.  
 RP SEQUENCE FROM N A.  
 RX MEDLINE: 91335768.  
 RA UPTON C., MAGEN J.L., SCHREIBER M., MCFADDEN G.;  
 RL VIROLOGY 184:370-382(1991).  
 CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO  
 REACH CELLULAR TARGET AND THEREBY DAMPENING THE POTENTIAL  
 CC ANTI-VIRAL EFFECTS OF THE CYTOKINE.  
 DR EMBL: M0511; G33210; -.  
 DR EMBL: A23729; E193442; -.  
 DR PIR: A0566; GOVZML.  
 DR HSSP; P19438; 1TNR.  
 DR PROSITE; PS00652; TNFR\_NGFR.  
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 326 PROBIN T2.  
 FT DOMAIN 27 186 4 X TNFR-CYS.

FT	REPEAT	27	62	TNF-CYS 1.
FT	REPEAT	63	104	TNF-CYS 2.
FT	REPEAT	105	147	TNF-CYS 3.
FT	REPEAT	148	186	TNF-CYS 4.
FT	CARBOHYD	66	66	POTENTIAL.
FT	CARBOHYD	181	181	POTENTIAL.
FT	CARBOHYD	205	205	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.
SQ	SEQUENCE	326 AA;	352.08 MN;	ZF-059A61 CRC32;
				Score 269; DB 10; Length 326;
				Best Local Similarity 33.8%; Pred. No. 5.03e-33; Mismatches 58; Indels 9; Gaps 8;
				Matches 47; Conservative
Db	40	ctscpgpsysarlrclagsatvcscnketfasnhanpacvssrgtghisessqcdkt	99	99
QY	41	CDKCPGTYKQHCAKWKWTCAPCPDHYTDSWHTSDCLYCSPPVKELOVVKQECNRT	100	100
Db	100	rdrvdcasagncyclkgqecrccapktcpaygvs-qhtrgqvltkcpyt-ydav	158	158
QY	101	HNRVCECKEGRY--LE-IEC-LKHRS-CPPGFVGVQAGTPERTVCKRCPDGFNET	154	154
Db	159	sstcttsssfyifsefnl	177	177
QY	155	SSKAPCRKHNINC-SV-FGL	171	171
				Score 205; DB 9; Length 415;
				Best Local Similarity 28.9%; Pred. No. 3.52e-32; Mismatches 92; Indels 11; Gaps 8;
				Matches 54; Conservative
Db	52	epmadvccsrcprpdpfrfvacsrsqdtvcktpphnsnehnwhnlstcqlcpc-dclvlgf	110	110
QY	34	ETHOLICDKCPPELYKLKHCWKWTCAPCPDHYTDSWHTSDCLYCSPVKE-LQY	92	92
Db	111	eavaajtsdkaecrcpamsccyldnaevcheerivlgcgpteeavtdsimdvny	170	170
QY	93	VK-QECNRTHNRVCBECKEGR--YLEIE--FCKHR-S-CPPGFV-VQAGTPERNVCK	143	143
Db	171	pckpgftqnssprarcqhtrcisqgivveaagtsydstichppngamliallsl	230	230
QY	144	RCPDGFSNETSKAPCRKHNINCVFGUHLIQKGNATNDIISNSSTOKCGGDIVTE	203	203
Db	231	vflift	237	237
QY	204	EAFERFA	210	210
				Score 205; DB 9; Length 415;
				Best Local Similarity 28.9%; Pred. No. 3.52e-32; Mismatches 92; Indels 11; Gaps 8;
				Matches 54; Conservative
RESULT	6			
ID	TNRC_MOUSE	STANDARD;	PRT;	415 AA.
AC	P0284			
DT	01-OCT-1996	(REL. 34, CREATED)		
DT	01-OCT-1996	(REL. 34, LAST SEQUENCE UPDATE)		
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)		
DE		LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.		
GN		TNCR.		
OS		MUS MUSCULUS (MOUSE).		
OC		EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC		EUTHERIA; RODENTIA.		
RN	[1]	SEQUENCE FROM N.A.		
RC		STRAIN=C57BL/10J; TISSUE=LUNG;		
RC		FORCE W.R., WILLIAMS-ABBOTT L., BROWNING J., HESSION C., TIZARD R.,		
RA		WARE C.F.,		
RL		SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDJB DATA BANKS.		
RN	[2]	SEQUENCE FROM N.A.		
RP		MEDLINE: 96163885.		
RX		NAKAMURA T., TASHIRO K., NAZARETA M., NAKANO T., SASAYAMA S.,		
RX		HONJO T.; GENOMICS 30:312-318(1995).		
CC		-!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN IMMUNE DEVELOPMENT.		
CC		-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC		-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.		
CC		EMBL: U21621; -.		
DR		EMBL: L38423; G60223; -.		
DR		EMBL: U30798; G106132; -.		
KW		RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.		
FT	SIGNAL	1	30	POTENTIAL.
FT	CHAIN	31	415	LYMPHOTOXIN-BETA RECEPTOR.
FT	DOMAIN	31	223	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	224	244	POTENTIAL.
FT	DOMAIN	245	415	CYTOSPLASMIC (POTENTIAL).
FT	REPEAT	42	81	4 X TNF-CYS.
FT	REPEAT	82	124	TNF-CYS 1.
FT	REPEAT	125	170	TNF-CYS 3.
FT	REPEAT	171	213	TNF-CYS 4.
FT	DISULFID	43	58	BY SIMILARITY.
FT	DISULFID	59	72	BY SIMILARITY.
FT	DISULFID	62	80	BY SIMILARITY.
FT	DISULFID	83	98	BY SIMILARITY.
FT	DISULFID	101	116	BY SIMILARITY.
RESULT	7			
ID	VT2_SFVKA	STANDARD;	PRT;	325 AA.
AC	P55943			
DT	01-MAY-1992	(REL. 22, CREATED)		
DT	01-MAY-1992	(REL. 22, LAST SEQUENCE UPDATE)		
DT	01-FEB-1994	(REL. 28, LAST ANNOTATION UPDATE)		
DE		TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).		
GN		T2.		
OS		SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).		
OC		VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE; LEPORIPOROVIRUSES.		
OC		[1]		
RN		SEQUENCE FROM N.A.		
RP		MEDLINE: 87321103.		
RX		UPTON C., DELANGE A.M., MCFADDEN G.; VIROLOGY 160:20-30(1987).		
RN	[2]	FUNCTION.		
RX		MEDLINE: 91207415.		
RX		SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., PARRAH T., UPTON C.,		
RA		MCFADEEN G., GOODWIN R.G.; BIOPHYS. RES. COMMUN. 176:335-342(1991).		
RL		BIOPHYS. BIOPHYS. RES. COMMUN. 176:335-342(1991).		
CC		-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPENTING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.		
CC		-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.		
CC		EMBL: M17433; -; NOT ANNOTATED_CDS.		
DR		EMBL: A23727; E19408; -.		
DR		PIR: B43692; BA33692.		
DR		HSSP: P19438; TNFR.		
DR		PROSITE: PS00532; TNFR_NGFR.		
KW		RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.		
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	325	PROTEIN T2.
FT	DOMAIN	27	186	4 X TNF-CYS.
FT	REPEAT	27	62	TNF-CYS 1.
FT	REPEAT	63	104	TNF-CYS 2.
FT	REPEAT	105	147	TNF-CYS 3.
FT	REPEAT	148	186	TNF-CYS 4.
FT	CARBOHYD	105	105	POTENTIAL.
FT	CARBOHYD	181	181	POTENTIAL.
FT	CARBOHYD	205	205	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.

SO	SEQUENCE	325 AA:	35132 MW;	C9D2C87B CRC32;
Query Match		9.1%; Score 260; DB 10; Length 325;		
Best Local Similarity	30.5%	Pred. No. 3.98e-31;		
Matches	51;	Conservative	31;	Mismatches 77; Indels 8; Gaps 5;
AC	cacsgpfgfaalrcgggnsntcspegdgtftastnhapacvscrpgtghsesqpcdr	99		
Db	40 cdkcpptgtylkohctakwktvcapcpdhywstsdeclycspvckelqvko	99		
OY	41 cdkcpptgtylkohctakwktvcapcpdhywstsdeclycspvckelqvko	100		
Db	100 hrvncestgngylkqngncrcaaptckpcgqyvs-ghtsdragtdloekcphtysdl	158		
OY	101 hnrvcckegry--l-eie-fclkrhrcscpgfgywqagtperntvckrcpdgffsn	154		
Db	159 sptercqtsfnysvgflnlpnctsctt-aghneviktkeftvtl	204		
OY	155 ssapkcrkhtncsvfglelltotkgnahdnicsgnsesto	201		
QY				
BLT	8 TNRC_HUMAN STANDARD; PRT; 435 AA.			
AC	P36941; DT 01-JUN-1994 (REL. 29, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).			
GN	TNFR.			
OS	HOMO_SAPIENS (HUMAN).			
OC	EUTHERIA; PRIMATES; MAMMALIA;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER.			
RX	MEDLINE: 93352281.			
RA	BAAENS M., CHAFANET M., CASSIMAN J.J., DEN BERGHE H., MARYNEN P.;			
RL	GENOMICS 16:214-218(1993).			
CC	-			
CC	- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN IMMUNE DEVELOPMENT.			
CC	- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
EMBL	L04270; G339762; -.			
MIM	600979; -.			
DR	HSSP; P19999; ICIG.			
DR	PROSITE; PS00652; TNFR_NGFR.			
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.			
FT	SIGNAL 1 30 POTENTIAL.			
FT	CHAIN 3 435 LYMPHOTOXIN-BETA RECEPTOR.			
FT	DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 228 248 CYTOPLASMIC (POTENTIAL).			
FT	DOMAIN 249 435 4 X TNFR-CYS.			
FT	REPEAT 42 81 TNFR-CYS 1.			
FT	REPEAT 82 124 TNFR-CYS 2.			
FT	REPEAT 125 168 TNFR-CYS 3.			
FT	REPEAT 169 211 TNFR-CYS 4.			
FT	DISULFID 43 58 BY SIMILARITY.			
FT	DISULFID 59 72 BY SIMILARITY.			
FT	DISULFID 62 80 BY SIMILARITY.			
FT	DISULFID 83 98 BY SIMILARITY.			
FT	DISULFID 101 116 BY SIMILARITY.			
FT	DISULFID 104 124 BY SIMILARITY.			
FT	DISULFID 126 132 BY SIMILARITY.			
FT	DISULFID 139 148 BY SIMILARITY.			
FT	DISULFID 142 167 BY SIMILARITY.			
FT	DISULFID 170 185 BY SIMILARITY.			
FT	40 40 BY SIMILARITY.			
QY				
BLT	9 TNRC_HUMAN STANDARD; PRT; 435 AA.			
AC	P36941; DT 01-JUN-1994 (REL. 29, CREATED)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	PROTEIN C22/B22 HOMOLOG.			
GN	GAR.			
OS	VARIOLA VIRUS.			
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPHOXVIRINAE; ORTHOPHOXVIRUSES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=INDIA-1967 / ISOLATE IND3.			
RX	MEDLINE: 93302281.			
RA	SCHELKINOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;			
RL	FERS LEIT. 319:80-83(1993).			
CC	- SIMILARITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.			
DR	EMBL; X69198; G457087; -.			
DR	EMBL; X67117; G516449; -.			
DR	D36858; D36588.			
DR	PIR; S35977; S35987.			
DR	PIR; S46888; S46888.			
DR	RSPB; P19438; 1TNR.			
DR	PROSITE; PS00652; TNFR_NGFR.			
KW	REPEAT.			
FT	DOMAIN 31 108 2 X TNFR-CYS.			
FT	REPEAT 31 66 TNFR-CYS 1.			
FT	REPEAT 67 108 TNFR-CYS 2.			
SO	SEQUENCE 349 AA; 38189 MW; 50D0B435 CRC32;			
Query Match		8.0%; Score 230; DB 10; Length 349;		
Best Local Similarity	35.4%	Pred. No. 6.9e-25;		
Matches	46;	Conservative	19;	Mismatches 58; Indels 7; Gaps 4;
DB	40 halcclecpptgtyasridskntqpcgsgstftsnnphipacslngcrgnsqnetrs	99		
OY	37 holcclecpptgtylkohctakwktvcapcpdhywstsdeclycspvckelqvko	96		
DB	100 cnthnrcicecpqycylkgsqckavsqtkcgqyvs-ghtsugdvicpcfcgty	158		
OY	97 cnrthrvcckegry--le- ie-fclkrhrcscpgfgywqagtperntvckrcpdgff	150		
DB	159 shtvssadkc 168			
OY	151 SNBTSSKAPC 160			
RESULT	10			
ID	TNRL_MOUSE	STANDARD;	PRT;	454 AA.
AC	P25118;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			
FT	CARBHYD			



FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 143 BY SIMILARITY.  
 FT DISULFID 146 158 BY SIMILARITY.  
 FT DISULFID 149 166 BY SIMILARITY.  
 FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 191 BY SIMILARITY.  
 FT DISULFID 185 195 BY SIMILARITY.  
 FT CARBOYD 154 54 POTENTIAL.  
 FT CARBOYD 151 151 POTENTIAL.  
 FT CARBOYD 201 201 POTENTIAL.  
 SQ SEQUENCE 461 AA; 50969 MW; 82F6B8B08 CRC32;

Query Match 7.7%; Score 220; DB 9; Length 461;  
 Best Local Similarity 33.8%; Pred. No. 7, 09e-23;  
 Matches 49; Conservative 22; Mismatches 63; Indels 11; Gaps 10;

Db 49 yahpkkinsicctkchqylvsdcaspgqgetvcvedkgftasasnhrvclscitcrke 108  
 31 YDEEISHQLCDKCPGTYLQHCTAK-WKTVCAPODPHYTDSWHTSDECILYSPVCKE 89  
 109 mfqveaispcakadmdvcgcknqfaylsethfqydcspofng tvtipokekantvn 167  
 QY 90 L-QYVKOECNRTHNRYCECK--E-GRYL-EIEP-CLKHRSOPPGFVVQAGTPERTVCK 143

Query Match 7.5%; Score 215; DB 6; Length 416;  
 Best Local Similarity 30.4%; Pred. No. 7, 20e-22;  
 Matches 45; Conservative 27; Mismatches 70; Indels 6; Gaps 6;

Db 36 okacnlgegvvqpcgvn-qtvcepcldsvtsvdsatespkpkctq-cvgllhsapcve 93  
 QY 41 CDKCPGTYLQHCTAKWVCAFPDHV YIDSHTSDECILYSPVCKELQVYKQECNR 99  
 Db 94 sddavercayqyqfaelsgsckecscicevqfqlmpcrdsqdtceecqegffdeanfv 153  
 QY 100 THNRVCECKEGRYL-EIE-FCLIKHSOPPGFVVQAGTPERTVCKRCPDGFFSNETSK 157

Db 154 dpcplpticeesenvk-e-tatstaek 180  
 QY 158 APRCRKHTNCVFGLLITOKGNATHDNIC 185

RESULT 12 STANDARD; PRT; 416 AA.

ID NGFR-CHICK P185;9  
 AC P185;9  
 DT 01-NOV-1990 (REL. 15, CREATED)  
 DT 01-NOV-1990 (REL. 15, LAST SEQUENCE UPDATE)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR) (GP80-LNGFR).  
 DE GALLUS GALLUS (CHICKEN).  
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; GALLIFORMES.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE-BRAIN;  
 RX MEDLINE; 90152140.  
 RA HEUER, J.G., FATEMIE-VAINTI, S., WHEELER, E.F., BOTHWELL, M.;  
 RL DEV. BIOL. 137:287-304(1990).  
 RA SHOTTER, E.M., RITCHARD, L.F.;  
 RL NEURON 2:1123-1134(1989).

[2]  
 RN SEQUENCE OF 21-416 FROM N.A.  
 RA MEDLINE; 90152140.  
 RA HEUER, J.G., FATEMIE-VAINTI, S., WHEELER, E.F., BOTHWELL, M.;  
 RL DEV. BIOL. 137:287-304(1990).  
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 CC NT-3, AND NT-4.  
 CC -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- PFM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNF- $\alpha$ -TYPE CYSTEINE-RICH REGION.  
 DR PIR: JN005; JN005.  
 DR PIR: A60504; A60504.  
 DR PROSITE; PS00652; TNFR\_NGFR.  
 DR PROSITE; PS50017; DEATH\_DOMAIN.  
 KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;  
 KW PHOSPHORYLATION; SIGNAL.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 416 NGF RECEPTOR.

FT DOMAIN 29 239 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 240 261 POTENTIAL.

FT DOMAIN 262 416 CITOPLASMIC (POTENTIAL).

FT DOMAIN 23 181 4 X TNFR-CYS.

FT REPEAT 23 57 TNFR-CYS 1.

FT REPEAT 58 100 TNFR-CYS 2.

FT REPEAT 101 140 TNFR-CYS 3.  
 FT REPEAT 141 181 TNFR-CYS 4.  
 FT DOMAIN 188 236 SER/THR-RICH.  
 FT DOMAIN 333 410 DEATH DOMAIN.

FT DISULFID 24 35 BY SIMILARITY.

FT DISULFID 35 49 BY SIMILARITY.

FT DISULFID 39 56 BY SIMILARITY.

FT DISULFID 59 75 BY SIMILARITY.

FT DISULFID 78 91 BY SIMILARITY.

FT CARBOYD 81 99 BY SIMILARITY.

FT DISULFID 101 114 BY SIMILARITY.

FT DISULFID 117 130 BY SIMILARITY.

FT DISULFID 120 138 BY SIMILARITY.

FT DISULFID 141 156 BY SIMILARITY.

FT DISULFID 159 172 BY SIMILARITY.

FT CARBOYD 162 180 BY SIMILARITY.

FT DISULFID 36 52 BY SIMILARITY.

FT CONFLICT 173 173 C -> Y (IN REF. 2).  
 FT CONFLICT 276 276 T -> K (IN REF. 2).  
 FT CONFLICT 396 396 N -> S (IN REF. 2).  
 FT CONFLICT 416 AA; 4D3F086A CRC32;

Query Match 7.5%; Score 215; DB 6; Length 416;  
 Best Local Similarity 30.4%; Pred. No. 7, 20e-22;  
 Matches 45; Conservative 27; Mismatches 70; Indels 6; Gaps 6;

Db 36 okacnlgegvvqpcgvn-qtvcepcldsvtsvdsatespkpkctq-cvgllhsapcve 93  
 QY 41 CDKCPGTYLQHCTAKWVCAFPDHV YIDSHTSDECILYSPVCKELQVYKQECNR 99  
 Db 94 sddavercayqyqfaelsgsckecscicevqfqlmpcrdsqdtceecqegffdeanfv 153  
 QY 100 THNRVCECKEGRYL-EIE-FCLIKHSOPPGFVVQAGTPERTVCKRCPDGFFSNETSK 157

Db 154 dpcplpticeesenvk-e-tatstaek 180  
 QY 158 APRCRKHTNCVFGLLITOKGNATHDNIC 185

RESULT 13 STANDARD; PRT; 427 AA.

ID NGFR\_HUMAN P0813;  
 AC P0813;  
 DT 01-AUG-1988 (REL. 08, CREATED)  
 DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR) (GP80-LNGFR).

GN NGFR.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.

RR SEQUENCE FROM N.A.  
 RX MEDLINE; 87051725.

RA JOHNSON, D., LANHAN, A., BUCK, C.R., SEHGAL, A., MORGAN, C., MERCER, E., BOTHWELL, M., CHAMO, R., CELL 47:545-554(1986).

CC -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3, AND NT-4.

CC -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- PFM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNF- $\alpha$ -TYPE CYSTEINE-RICH REGION.

DR EMBL: M14764; G189205; PIR: A25218; GQUN.

DR HSSP; P19438; ITNR.

DR MM; 162010; -

DR PROSITE; PS00652; TNFR\_NGFR.

DR PROSITE; PS50017; DEATH\_DOMAIN.

KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; PHOSPHORYLATION; SIGNAL.

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-1 - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC

FT

SIGNAL

1

28

NGF RECEPTOR

(POTENTIAL).

EXTRACELLULAR

(POTENTIAL).

CYTOPLASMIC

(POTENTIAL).

4 X TNFR-CYS.

TNP-CYS 1.

TNP-CYS 2.

TNFR-CYS 3.

TNFR-CYS 4.

DEATH DOMAIN.

BY SIMILARITY.

Query Match 7.4%; Score 213; DB 6; Length 427;  
 Best Local Similarity 34.9%; Pred. No. 1 81e-21; Indels 19; Mismatches 60; Gaps 5; Matches 45; Conservative

Db 44 ckacnlggeqvacpgcan-qtvcepcldasvtfsdvvsatepkcpte-cvgqlsmaspce 101  
 41 CDKOPPGYIQLKHTQHCTAKWKTVCAPCPHY-YTDSWHSDECILYCPVCKELOVYKQECNR 99

Qy 102 addavrcayggyqdetgrceacrvceagsdvlvsfqscqdkqntvcecpagtyse deanhv 161  
 100 THRNVCCEKEGRYI-EI-EFCLKRSCPPGFGVWQACTPERNTVCKRCPDGFFSNETSSK 157

Db 162 dpcipctvc 170  
 Qy 158 APCRKHTNC 166

RESULT 14 ID NEPR RAT STANDARD; PRT; 425 AA.  
 AC P0174; DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)  
 DE 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GBBO-LNGFR).

GN RATTUS NORVEGICUS (RAT); OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1] SEQUENCE FROM N.A.  
 RP MEDLINE; 87115859.  
 RX RADEKE M.J.; MISKO T.P.; HSU C.; HERZENBERG L.A.; SHOOTER E.M.;  
 RL NATURE 325:593-597(1987).  
 RN [2] SEQUENCE OF 1-22 FROM N.A.  
 RP TISSUE=LIVER;  
 RX MEDLINE; 93077038.  
 RA METSIS M.; TIMISKI T.; ALLIKMETS R.; SAARMA M.; PERSONN H.;  
 RL GENE 121:247-254 (1992).  
 CC -1 - FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 NT-3, AND NT-4.  
 CC SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.  
 CC -1 - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

RESULT 15 ID FAS\_A\_BOVIN STANDARD; PRT; 323 AA.  
 AC P51867; DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1995 (REL. 34, LAST ANNOTATION UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST SURFACE ANTIGEN FAS)  
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS) (APO-1 ANTIGEN) (CD95).  
 DE APTL OR FAS.  
 GN OS BOS TAUREUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTYLIA.  
 RN [1] SEQUENCE FROM N.A.  
 RP MEDLINE 96226401.  
 RX YOO J.; STONE R.T.; BEATTIE C.W.;  
 RL DNA CELL BIOL. 15:227-234(1996).  
 CC -1 - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDIATES CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE

Query	Match	Score	Length
Qy	hafccgcpckrgnagckrdgtpevcilsgneytdkskhsdkcires icdeehgile	188	31
Qy	:    :    :    :    :    :    :    :    :    :    :    :	111	6
Qy	HOLCDKCPGTYLQHCTAKKTV-CAPCP-HYVPSWHSPECYCSPCKELO-Y	92	6
Db	veqncctrntkrcknnfcnssspccchpnptctceigliefktptsnck	163	6
Db	_ :    :    :    :    :    :    :    :    :    :    :	163	6
Qy	VKOECNRTHNRVCECKEGRYLEIEFCLKHRSPP-GFGVWQAGTPERNTVCK	143	6

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